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The Genographic Project: insights into Western/Central European variation

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The spread of *Homo sapiens* out of Africa and the subsequent continent colonisations and migrations have been reconstructed through the analyses of data reported by several disciplines, such as paleoanthropology, archaeology, linguistics and genetics. The joint effort of these disciplines has allowed having a broad knowledge about the tempo and mode of the origin of our species and the major colonisations at a continental level (Jobling *et al.*, 2004). However, some local migration routes, especially those within continents, are far for been completely understood.

In order to shed light to the reconstruction of human migrations through the analysis of genetic markers, National Geographic and IBM, with the participation of the Waitt Family Foundation, have launched the Genographic Project (http://genographic.nationalgeographic.com). This international project aims to provide genetic data in order to reconstruct human movements through the analysis of uniparental genomes (mitochondrial DNA and Y chromosome). The project has three main subprojects: the public participation, the legacy fund, and research project.

The public part of the project aims to encourage general public to know more about their own ancestors. Each individual interested in knowing his/her deep ancestry along a single line of direct descent (maternal or paternal) can acquire a kit that is sent to his/her home. In about eight weeks, the results of the maternal or paternal markers will be deposited anonymously in the webpage of the Genographic Project and the individual can access to the data with his/her code. The sequence of the first hypervariable region of the mitochondrial DNA or some STRs and SNPs of the Y chromosome are provided to the participants in order to classify their lineage into the human phylogenetic tree and the information of the migration history of this particular branch is also available for the participant. The funds collected in this part of the public participation support the rest of the project. The participants can also introduce their data to an anonymous general database that can be used for global analyses. In this way, a global analysis of more than 78,000 mitochondrial results of the database has been published (Behar *et al.,* 2007).

The Legacy Fund, a subproject of Genographic, through the extension of grants, aims to empower indigenous and traditional peoples by supporting locally-led efforts that can also raise global awareness about the cultural loss indigenous and traditional communities face.

Finally, the third part of the Genographic Project is the research project. This part aims to unravel the migration history of the human species at a population level. Several groups of scientists, one in each continent, are collecting samples representative of the geographical regions in order to have a general coverage of the human variation. The goal of the project is to collect a total of 100,000 samples to unravel major and minor migrations of the human species.

Within Western/Central Europe, we are proceeding with the sample collection and the first analyses of the results. These analyses will allow us to provide a finer resolution of

the migrations within Europe and neighbouring geographic areas. More than 5,000 samples have already been collected and we are proceeding with the analyses of the Y-chromosome and mitochondrial DNA. The main questions to answer in Europe are the ones that have been posed for several years and not totally answered by genetic markers. To what extent the current European gene pool has been influenced by both Palaeolithic and Neolithic migrations? What was the role of the Last Glacial Maximum refugees and the subsequent recolonization of the continent? Was the Neolithic migration homogeneous across Europe? Can we correlate differences in archaeological Neolithic sites (linear pottery culture in Central Europe and impressed ware pottery in the Mediterranean) with different migratory waves? What was the influence of more recent migrations in the European genetic landscape? In order to address these questions we will use massive sample sizes, high resolution markers in the uniparental genomes, as well as standardized methods of analysis. We have been collaborating with other regional centres within the Genographic Project in order to address local genetic issues. In this way, we have demonstrated the genetic impact of the Crusaders in the Near East using Y-chromosome markers (Zalloua et *al.,* 2008), or the genetic impact of Phoenicians in the Mediterranean (Zalloua *et al.,* 2008).

With the Genographic Project, we aim to shed light to the migration history of our species and test some hypotheses posed by different disciplines. We hope to use the present genetic knowledge to provide in the future the answers about our remote past.

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